Amendments to the Specification:

Please amend the Title on page 1 at line 1 of the Specification as follows:

~~ErbB4-CO-CRYSTAL~~

METHOD OF INHIBITOR DESIGN USING A 3-D STRUCTURE OF ErbB4 KINASE

Please amend the fourth full paragraph on page 7 of the Specification as follows:

Table 2 is a table of the atomic structure coordinate data obtained from X-ray diffraction from the liganded ErbB4K crystal form. SEQ ID NO. 3 lists the amino acids of Table 2 in the order in which they are listed in the table.

Please amend the second full paragraph on page 44 of the Specification as follows:

A combination of limited proteolysis and modeling was used to define the construct for structural studies. First, the cytoplasmic domain of ErbB4 (residues 690-1309) was ligated in frame behind a 6xHis tag (MKKGHHHHHHG; SEQ ID NO:4) in a pFastBac1 vector (Invitrogen). The cloned sequence was identical to that reported in GENBANK (L07868).

Please amend the paragraph beginning on the bottom of page 54 of the Specification as follows:

The method measures the ability of the isolated enzyme to catalyse the transfer of the γ-phosphate from ATP onto tyrosine residues in a biotinylated synthetic peptide (biotin-Ahx-RAHEEIYHFFFAKKK-amide). The sequence of this peptide is shown in SEQ ID NO:5. Reactions were performed in 96-well polystyrene round-bottom plates in a final volume of 45 μL. Reaction mixtures contained 50 mM MOPS (pH 7.5), 2 mM $MnCl_2$, 10 μM ATP, 0.125 μCi [γ-^{33}P] ATP per reaction, 2 μM peptide substrate, and 1mM dithiothreitol. Reactions were initiated by adding 1pmol (20nM) per reaction of the indicated enzyme. The reaction was allowed to proceed for 15 minutes, terminated and quantified using a scintillation proximity assay procedure as described in McDonald, O.B., Antonsson, B., Arkinstal, S., Marshall, C.J., and Wood, E.R. (1999) *Analytical Biochemistry*, **268**, 318-329.